

FT CONFLICT 285 288 GORO -> ASSE (IN REF. 2).
 FT CONFLICT 326 329 RROK -> POE (IN REF. 2).
 FT CONFLICT 365 374 KPVKPTHS -> NPLSSSRTP (IN REF. 2).
 FT CONFLICT 785 785 S -> N (IN REF. 2).
 SQ SEQUENCE 1275 AA; 142589 MW; 91CFCD9896981 CRC64;

Query Match 5.0%; Score 198.5; DB 1; Length 1275;
 Best Local Similarity 19.9%; Pred. No. 2.2e-06;
 Matches 130; Conservative 100; Mismatches 251; Indels 171; Gaps 27;

QY 153 MACSTDYRGSALHIAIEKRSLOCVKLVENGAVNARACGRFGKGCCTFYEGELP 212
 DB 62 NINCTDPMNR-SALISAIENENFDLWVLEHNIEV-----GALLHAISEEX 108
 QY 213 LSLAACKQMDVSYLLENPHQASLOADDSQNTV---LHALVMSDMSAENIALVTSM 269
 DB 109 VEAVEELLQWEETNH---KEGQYSWEADVRSKSTFTVDITPLILAAHRNNVEILKI--- 162
 QY 270 YDGLLOAGARL-----CPTVOLED-----TRNLODLPKLAKCKG 306
 DB 163 ---LDRGATLPRPHDYKCGDCVTSQTTDSLRSOSRINATRALSASSLALSSRDY 219
 QY 307 IEIFRIILOREFSGLSHLSKRTKFTWCYGPVRSYLDAS--VDSCEENVLEIIFRCKS 364
 DB 220 LTFVFO--LSWELKRLQAMESEFRAE-YTEMROWVODFGTSLDHARTSMELVNLNHE 276
 QY 365 P-----HHRMNVLEP-LNKLQAKWLLLPKF----- 381
 DB 277 PSNDIMCLOROTLEKLAIRYKQTFVANHVNQDLAIIWDGLPGRKQASQOQLMD 336
 QY 392 FLNPLNLIYMEFTAVVYHQPTLKKOAPHLKAEVNSMLLGHILILGIGIYLLVGOL 451
 DB 337 VVVLGGSFPIYSKLTLAPDSGAKFMKRFVKFITHSCSYM--FLMLLGAASLKVQI 394
 QY 452 ---WTF---WRRH-----VF-----I 461
 DB 395 TPELLAFPMWLTMLMDMRKHERGSLRPIELAITIYIMALIFEELKSLVSDGFEYIMDL 454
 QY 462 W--ISFIDSFEFLF--QALLTVSQCVCFLAIEWYL-----PLVVS-----A 502
 DB 455 WNIIVDISSNMFYTWILCRATAVIVHRDIFWFGIDYPRPREHMPDPDLSEGAFAAG 514
 QY 503 LVLGWNLILYTRGFQHTGIYSVIOKVIILDLRLFLILVLFEGFAVALVSLSEAMR 562
 DB 515 MVSYSKIVHIEFINHIGRPLQVSLGRMII-DIKKFFITVLVFAFG---CGLNQLMW 570
 QY 563 PEAPTPNATESYQVPEGDESGNGA---QYRGLLEASLELFKFTTIGMELAFQE--- 614
 DB 571 -VAELEKNCYHLHPVADFDDEKACTIWRFRSNLFTSOSLFWASFGIADLVSPDLAG 629
 QY 615 -OLHFEGVLLLLLAYVLLLYILLMLLALMSETVNSVATDSMTWKLOKA 665
 DB 630 IKSTFRMALLMGYSYVNIITVLLMLLMMSSNSYQIISERADTEWKFARS 681

RESULT 3
 TRPL_DROME STANDARD; PRT; 1124 AA.
 AC P48994;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 30-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRANSLATION-RECEPTOR-POTENTIAL LIKE PROTEIN.
 GN TRPL.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;

RX MEDLINE-92232293; PubMed-1314616;
 RA Phillips A.M., Bull A.L., Kelly L.E.;
 RT "Identification of a Drosophila gene encoding a calmodulin-binding
 protein with homology to the trp phototransduction gene.";
 RL Neuron 8:631-642(1992).
 CC -1- FUNCTION: BINDS CALMODULIN. SUGGESTED TO MEDIATE CALCIUM ENTRY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PERMEANT CHANNEL.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
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CC EMBL: M8185; AAA28979.1; -
 DR Flybase; FBgn005614; trpl.
 DR InterPro; IPR002110; -
 DR InterPro; IPR002153; -
 DR Pfam; PF00023; ank; 2.
 DR PRINTS; PR01097; TRANSRECEPT.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW Calmodulin-binding; Vision; Ank repeat; Repeat.
 FT TRANSMEM 341 361 POTENTIAL.
 FT TRANSMEM 374 394 POTENTIAL.
 FT TRANSMEM 432 452 POTENTIAL.
 FT TRANSMEM 513 533 POTENTIAL.
 FT TRANSMEM 549 569 POTENTIAL.
 FT TRANSMEM 609 629 POTENTIAL.
 FT TRANSMEM 646 666 POTENTIAL.
 FT REPEAT 78 107 ANK 1.
 FT REPEAT 152 181 ANK 2.
 FT DOMAIN 710 727 CALMODULIN-BINDING (POTENTIAL).
 FT DOMAIN 809 825 CALMODULIN-BINDING (POTENTIAL).
 SQ SEQUENCE 1124 AA; 127697 MW; E14796D5A2C10BD CRC64;

Query Match 4.9%; Score 197.5; DB 1; Length 1124;
 Best Local Similarity 19.7%; Pred. No. 2.2e-06;
 Matches 162; Conservative 130; Mismatches 281; Indels 249; Gaps 38;

QY 131 VNACIPLQLQIDRDSGNPOPL-----VNACSTD 159
 DB 25 VGCCVPL-----GLPQLLEKKFLLAVERGMPNVRILQALRHHQINIMCMP 77
 QY 160 YRGSALHIAIEKRSLOCVKLVENG-----ANVHARAC-----GRFGK 201
 DB 78 L--GRALFLAIDENLLEWVELLVVGVETKQALLHAINAEFEVALLLEHLLYKKG 135
 QY 202 Q-----GTCTFYGEL-PLSLAACKQMDVSYLLEN-----PH-----QPSL 238
 DB 136 EPYSMQKVDINTAFAPDITPLMLAAHKNFELIRLLDRGAAPVPVPHDRCGCECVRL 195
 QY 239 QATDSQNTVH-----ALVMSIDNSAENIALVSMVDGLQACARLCPYQLD 288
 DB 196 TAEDSLRHSISRNYIRALCSPLICLSTNDSSSTAFOULSWELRNALTEQDEKSYMDL 255
 QY 289 IRNLQ-----DLPLPLKLAKEGKIEI-----FRHILQREFSGLSHLSKRTKFTWC 332
 DB 256 RRCQCFANVDLDQRTSNELAILWYDPQMSYERGDMSLRLVQALSYQKKV--A 313
 QY 333 YGFVRSYL---YDLASVDSCEENVLEIIFRCKSPHRHNVLEPLNKLK-----QAK 383
 DB 314 HSNIDQLSSIMWD--GLPGRKRSIVDKVI--CIA-----QVAVLEPLCLLYMCAPNCR 365

OY	384	MDLLIPPEFLFCLN----	LIVIEIFFAVA-----	THQPTLKROAPHLEAEVGN	422
Dd	366	TGOLMRKPRFMKFLHASSYLFELFILLYSQRRDDPFVITFGTTKKKELAEOELRQNG			425
OY	430	SMLLTGHILLGGIYLLVLGSQLMWFWKRHRVFIWISFIDSYFEILELFOALL--TVVSQVL			487
Dd	426	----TPSKLETILVMVY----	IGFVMEVOGEIPAVGMKSYLELRNMNFIDFLRNSLYSVM		477
OY	488	CFLAIEW-----	YLPR-----	LVLSALVLGHLNLTYTRBQG	518
Dd	478	CLRPAFYIQOATEIARDPOMAYVIREKHWFDFOLIABGLFAANVFSAKLKVHLFSINP			537
OY	519	HTGIYSVAIOKVIILRDRLRLIYLVIFEGFAVALISLQEW-----	REAPATGPNAUT		572
Dd	538	HILGFLQSLSGRMVY-DLVKFFFIYTLVAFNA--CGLOMLMYFALEKSKCYLPG--			591
OY	573	ESVOPMGQEDEGNGA-----	OYRGILEASLELFKFTIGCEL-----	AFOQLHFR	619
Dd	592	-----GEADMGSHGDSCMKMRFRGULFESSQSILFPWASFVGWGDDPELGSIKSYTRFW			644
OY	620	GMYLLLLLAYLVLYILLMLTAISEYNVATSWSIWKLOAKAISVLEMENGYMCR			679
Dd	645	G-LLMGCSYVINIVYLLMLLTAMMSNSTAMIDEHSDETCKFAR-----	TLKMSY		694
OY	680	KKORAGVWLVTGTRPKDSSPDPERMCFRV-----	BEVNWASNEQTLLPLC		722
Dd	695	FEDSA-----TLPPFNVLVPVKMWIRIFRKSSKTIDRSKKRKKEQSEVDIMNRSLV			750
OY	723	EDPSGAGVPTLENPVLASPKDE--DGASENNYPVOLLO			762
Dd	751	W-RYVAAMHKRFEN----	NPEVEDLINEVKSETINTRYEMLE		787
RESULT	4				
TRPL_MOUSE	ID	TRPL_MOUSE	STANDARD;	PRT;	809 AA.
AC	061056:	035722;			
DT	01-OCT-2000	(Rel. 40,	Created)		
DT	01-OCT-2000	(Rel. 40,	Last sequence update)		
DT	01-OCT-2000	(Rel. 40,	Last annotation update)		
DE	TRANSIENT RECEPTOR POTENTIAL CHANNEL 1 (TRANSIENT RECEPTOR PROTEIN 1)				
DE	(TRP) (TRP-RELATED PROTEIN 1).				
GN	TRPC1 OR TRRP1 OR TRPI.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090;	[1]				
NP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.				
RC	TISSUE=Insulinoma;				
RX	MEDLINE=97307994; PubMed=9165220;				
RA	Sakura H., Ashcroft F.M.;				
RT	"Identification of four trpl gene variants murine pancreatic beta-				
RT	cells.";				
RL	Diabetologia 40:528-532(1997).				
RN	[12]				
RP	SEQUENCE FROM N.A. (BETA ISOFORM).				
RC	TISSUE=Lens epithelium.				
RA	Rae U.L.;				
RT	"Ion channels in lens epithelia.";				
RL	submitted (OCT-1999) to the EMBL/Cenbank/DBJ databases.				
NP	[13]				
RP	SEQUENCE OF 551-615 FROM N.A.				
RX	MEDLINE=96234226; PubMed=8646775;				
RA	Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,				
RA	Birnbauer L.;				
RT	"Trp, a novel mammalian gene family essential for agonist-activated				
RT	capacitative Ca ²⁺ entry.";				
CC	Cell 85:661-671(1996).				
CC	-I- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).				
CC	SEEMS TO FORM A CALCIUM PERMEANT CHANNEL.				
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).				
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; AREE				

CC PRODUCED BY ALTERNATIVE SPLICING.
CC -I- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
CC -I- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC -----
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CC	DR	EMBL	U73625; AAB50622.1; -	POTENTIAL.
DR	EMBL	U95167; AAC53162.1; -	POTENTIAL.	
DR	EMBL	AF191551; AAF05725.1; -	POTENTIAL.	
DR	EMBL	U40980; AAC52699.1; -	POTENTIAL.	
DR	MED	MGI:109528; Ttrpl.	POTENTIAL.	
DR	InterPro	IPR002111; -	POTENTIAL.	
DR	InterPro	IPR002153; -	POTENTIAL.	
DR	PRINTS	PRO1097; TRNSRECEPTP.	POTENTIAL.	
KW	Ionic channel; Transmembrane; Ion transport; Calcium channel;			
KW	ANK repeat; Repeat; Alternative splicing.			
FT	TRANSMEM	367	387	POTENTIAL.
FT	TRANSMEM	403	423	POTENTIAL.
FT	TRANSMEM	432	452	POTENTIAL.
FT	TRANSMEM	512	532	POTENTIAL.
FT	TRANSMEM	556	576	POTENTIAL.
FT	TRANSMEM	603	623	POTENTIAL.
FT	TRANSMEM	633	653	POTENTIAL.
FT	REPEAT	62	91	ANK 1.
FT	REPEAT	99	128	ANK 2.
FT	REPEAT	174	203	ANK 3.
FT	CARBOHYD	86	86	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	110	110	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	303	303	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	322	322	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	597	597	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	126	159	MISSING (IN ISOFORM BETA).
QO	SEQUENCE	809 AA;	92727 MW;	DED8377D5C538CD CRC64;

Query Match	4.0%:	Score 159:	DB 1:	Length 809:
Best Local Similarity	18.8%:	Pred. No. 0.00083:		
Matches 142:	Conservative 115:	Mismatches 249:	Indels 248:	Gaps 34:
OY	86	GVPEDLAQLPEY-----LSKTSKYLTDSEYTESGTGKTLMAKAV-----	124	
Db	2	GAPPPSPPLPSMAMMALPYTDLSGVSSSSLSPPSSSSPMEVMAIKQVREKVENT	61	
OY	125	LNKLDVNAAC-----LPLLOIDROSGNQPLVNACTDYRYGHALHIAIEKRSLO	177	
Db	62	LNKEKFLIACCKGKYWMVKITL-ENSSGD--LNLNCVQ-VLGRNAVTTIENESLD	114	
OY	178	CVKLLVENGAN-----VHARACG-----RFQKGQGTFFEGE-----	210	
Db	115	ILQLLLDVCGCSADALLVAIDSEYVAGDILLNHRPKSSRPTLYKLMERIQNPYSTTM	174	
OY	211	--LPLSLAACKQMDVVSYLE-----NPH-----	233	
Db	175	DVAPEVILIAHNNNYEILITMLLKQOVSLPKPRAVGOECLCSAKNKKSLRHSREFLDIYR	234	
OY	234	---QPASIQARDSQGNPLHALVAMISD-----NSAENIALVTSWYDGLLOGA	278	
Db	235	CLASDALMLTEE--DPLIRAFELISADIKELSLVEVERNDYEELARCKKFAKDILMOA	292	
OY	279	RLCFVQLLEDIRN-----LQDLPLPLAAKEGKIETLFRHLLQREFSGLS	322	
Db	293	R--NSRELEVLINHTSSDEPLDKRGLLEERNMLSLKAIKAYN-----QKEF-----	337	
OY	323	HLSKRFTWCYGPVAVRSIYDLASVDSCEANSVLELIAFHCKSPHRRH-----NMLE--	374	
Db	338	-----VSQSNCO--FLNTYWGQSGNSGRNRKCTCKRMIVLVLG	374	

QY 375 ---PLNKL-----QAKMDLIPKFLNCLNLYMFIT-----AVAYHOPTEKQAA 420
 Db 375 IMPVASTLCYLLAKSKQSFRIHTHPMKFLINGASFTLLNLXSLVYNEK----- 428
 QY 421 PHKAEVNGSMILGTHILLIGITVYLQOLVFMRRHVFIMSTDSYFE-----ILFL 475
 Db 429 ---KNTMGALRERIDILL-----WIMIMSDIKR---LWEGIEDELFEESRNLSFV 477
 QY 476 FQA---LLTVASOVLCFLA-----EM---YLPLVASLVGMLNLLYTRGQHIGITS 524
 Db 478 MNSLYLATFALVAVAHNKHDFADRKMDAFHPTLVAEGLFAFANVLSYLRLEFMTTSS 537
 QY 525 VM-----IQKVLIRDLRLFLIYVLFEGFAVALVSLQEAHPPEAPTPGNATESYQPM 579
 Db 538 ILGPIQISGMQMLQDGRKLGMLFLVLFSTYGLTOLYKGY-----TSKEOKDCYGIC 592
 QY 580 GQEDGNGAOYRGILEASLELKEFTIGMGEALF-----OGLHFRGNVLLLLIAYVL 631
 Db 593 EDOOSNDT---FHSFICTCFALFWYIFSLAHVAIFVTRFSYGEELQSFVAV--IVGTANN 647
 QY 632 LTVILLNMLIMSETVNSVATDSMSIKLQKA 665
 Db 648 VVVYVLTKLVLALHKSFOLIANHEKEMKFAKA.681

RESULT 5
 ANK2_HUMAN
 ID ANK2_HUMAN STANDARD: PRT: 3924 AA.
 AC 001484; 001485; (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
 GN ANK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain stem;
 RX MEDLINE=94073409; PubMed=8253844;
 RA Chan W., Kordeli E., Bennett V.;
 RT "440-kD ankyrinB: structure of the major developmentally regulated
 RT domain and selective localization in unmyelinated axons.";
 RL J. Cell Biol. 123:1463-1473(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
 RC TISSUE=Brain stem;
 RX MEDLINE=91302466; PubMed=1833053;
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
 RT "Isolation and characterization of cDNAs encoding human brain
 RT ankyrins reveal a family of alternatively spliced genes.";
 RL J. Cell Biol. 114:241-253(1991).
 RN [3]
 RP REVISIONS.
 RA Carpenter S.;
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE=92009921; PubMed=1833308;
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 RT ankyrin gene.";
 RL Genomics 10:858-866(1991).
 CC -!- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
 CC SKELETAL ELEMENTS. THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
 CC BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP95,
 CC AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
 CC DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
 CC THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CC CELLS THROUGHOUT THE BRAIN.
 CC -!- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
 CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
 CC AND FUNCTION (POTENTIAL).
 CC -!- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 CC EMBL: Z26634; CAB42644.1; -
 CC EMBL: X56957; CAA40278.1; -
 CC EMBL: X56958; CAA40279.2; -
 CC EMBL: M37123; AAA62828.1; -
 CC PIR: S14533; S14533.
 CC PIR: A39643; A39643.
 CC PIR: B39643; B39643.
 CC PIR: S14569; S14569.
 CC HSP: 000420; LAMC.
 CC MIM: 106410; -
 CC InterPro: IPR000488; -
 CC InterPro: IPR000906; -
 CC InterPro: IPR002110; -
 CC Pfam: PF00791; Z05; 1.
 CC Pfam: PF00023; ank; 22.
 CC Pfam: PF00531; death; 1.
 CC PROSITE: PS50088; ANK_REPEAT; 20.
 CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 CC PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC KWSkeleton: Alternative splicing; Repeat; ANK repeat;
 CC KW Phosphorylation; Multigene family;
 FT REPEAT 63 92
 FT REPEAT 96 125 ANK 1.
 FT REPEAT 129 158 ANK 2.
 FT REPEAT 162 191 ANK 3.
 FT REPEAT 193 220 ANK 4.
 FT REPEAT 232 261 ANK 5.
 FT REPEAT 265 294 ANK 6.
 FT REPEAT 298 327 ANK 7.
 FT REPEAT 331 360 ANK 8.
 FT REPEAT 364 393 ANK 9.
 FT REPEAT 397 426 ANK 10.
 FT REPEAT 430 459 ANK 11.
 FT REPEAT 463 492 ANK 12.
 FT REPEAT 496 525 ANK 13.
 FT REPEAT 529 558 ANK 14.
 FT REPEAT 562 591 ANK 15.
 FT REPEAT 595 624 ANK 16.
 FT REPEAT 628 657 ANK 17.
 FT REPEAT 661 690 ANK 18.
 FT REPEAT 694 723 ANK 19.
 FT REPEAT 727 756 ANK 20.
 FT REPEAT 760 789 ANK 21.
 FT REPEAT 793 822 ANK 22.
 FT REPEAT 825 854 ANK 23.
 FT REPEAT 857 886 ANK 24.
 FT REPEAT 889 922 ANK 25.
 FT REPEAT 925 958 ANK 26.
 FT REPEAT 961 994 ANK 27.
 FT REPEAT 997 1030 ANK 28.
 FT REPEAT 1033 1066 ANK 29.
 FT REPEAT 1069 1102 ANK 30.
 FT REPEAT 1105 1138 ANK 31.
 FT REPEAT 1141 1174 ANK 32.
 FT REPEAT 1177 1210 ANK 33.
 FT REPEAT 1213 1246 ANK 34.
 FT REPEAT 1249 1282 ANK 35.
 FT REPEAT 1285 1318 ANK 36.
 FT REPEAT 1321 1354 ANK 37.
 FT REPEAT 1357 1390 ANK 38.
 FT REPEAT 1393 1426 ANK 39.
 FT REPEAT 1429 1462 ANK 40.
 FT REPEAT 1465 1498 ANK 41.
 FT REPEAT 1501 1534 ANK 42.
 FT REPEAT 1537 1570 ANK 43.
 FT REPEAT 1573 1606 ANK 44.
 FT REPEAT 1609 1642 ANK 45.
 FT REPEAT 1645 1678 ANK 46.
 FT REPEAT 1681 1714 ANK 47.
 FT REPEAT 1717 1750 ANK 48.
 FT REPEAT 1753 1786 ANK 49.
 FT REPEAT 1789 1822 ANK 50.
 FT REPEAT 1825 1858 ANK 51.
 FT REPEAT 1861 1894 ANK 52.
 FT REPEAT 1897 1930 ANK 53.
 FT REPEAT 1933 1966 ANK 54.
 FT REPEAT 1969 2002 ANK 55.
 FT REPEAT 2005 2038 ANK 56.
 FT REPEAT 2041 2074 ANK 57.
 FT REPEAT 2077 2110 ANK 58.
 FT REPEAT 2113 2146 ANK 59.
 FT REPEAT 2149 2182 ANK 60.
 FT REPEAT 2185 2218 ANK 61.
 FT REPEAT 2221 2254 ANK 62.
 FT REPEAT 2257 2290 ANK 63.
 FT REPEAT 2293 2326 ANK 64.
 FT REPEAT 2329 2362 ANK 65.
 FT REPEAT 2365 2398 ANK 66.
 FT REPEAT 2401 2434 ANK 67.
 FT REPEAT 2437 2470 ANK 68.
 FT REPEAT 2473 2506 ANK 69.
 FT REPEAT 2509 2542 ANK 70.
 FT REPEAT 2545 2578 ANK 71.
 FT REPEAT 2581 2614 ANK 72.
 FT REPEAT 2617 2650 ANK 73.
 FT REPEAT 2653 2686 ANK 74.
 FT REPEAT 2689 2722 ANK 75.
 FT REPEAT 2725 2758 ANK 76.
 FT REPEAT 2761 2794 ANK 77.
 FT REPEAT 2797 2830 ANK 78.
 FT REPEAT 2833 2866 ANK 79.
 FT REPEAT 2869 2902 ANK 80.
 FT REPEAT 2905 2938 ANK 81.
 FT REPEAT 2941 2974 ANK 82.
 FT REPEAT 2977 3010 ANK 83.
 FT REPEAT 3013 3046 ANK 84.
 FT REPEAT 3049 3082 ANK 85.
 FT REPEAT 3085 3118 ANK 86.
 FT REPEAT 3121 3154 ANK 87.
 FT REPEAT 3157 3190 ANK 88.
 FT REPEAT 3193 3226 ANK 89.
 FT REPEAT 3229 3262 ANK 90.
 FT REPEAT 3265 3298 ANK 91.
 FT REPEAT 3301 3334 ANK 92.
 FT REPEAT 3337 3370 ANK 93.
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 FT REPEAT 10000

OY 377 ----NKLQAKMDLIPKFLNLIYMFETAVAYOPLTKQOAPHLKA-----EY 427
 DB 572 AVHNNLDIVK--LLPRL-----GGSPHSPAMNGTPPLHIAKQOIEV 613
 OY 428 GNSMLTIG 435
 DB 614 ARSLLOYG 621
 RESULT 8
 TRP3_HUMAN STANDARD: PRT: 848 AA.
 ID TRP3_HUMAN
 AC Q13507: 000593: Q15660;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TRANSIENT RECEPTOR POTENTIAL CHANNEL 3 (TRP-3).
 GN TRP3 OR TRP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96234226; PubMed=8646775;
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
 RA Birnbaumer L.;
 RT "Trp, a novel mammalian gene family essential for agonist-activated
 RT Cell 85:661-671(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97358541; PubMed=9215637;
 RA Xu X.-Z.S., Li H.-S., Guggino W.B., Montell C.;
 RT "Coassembly of TRP and TRPL produces a distinct store-operated
 RT conductance." J. Biol. Chem. 272:1155-1164(1997).
 RL [3]
 RN SEQUENCE OF 632-747 FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=96003837; PubMed=7568191;
 RA Wes P.D., Chevesich J., Jeromin A., Rosenberg C., Stetten G.,
 RA Montell C.;
 RT "TRP1, a human homolog of a Drosophila store-operated channel.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:9652-9656(1995).
 CC -1- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).
 CC -1- SEEMS TO FORM A CALCIUM PERMEANT CHANNEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
 CC -----
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 CC -----
 CC EMBL: U47050; AAC51653.1;
 DR EMBL: Y13758; CA674083.1;
 DR EMBL: X89068; CAA61448.1;
 DR MIM: 602345;
 DR InterPro: IPR002110;
 DR InterPro: IPR002111;
 DR InterPro: IPR002153;
 DR Pfam: PF00023; ank; 2.
 DR PRINTS: PRO1097; TRANSRECEPT.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW ANK repeat; Repeat; Glycoprotein.
 FT TRANSMEM 350 370 POTENTIAL.
 FT TRANSMEM 382 402 POTENTIAL.

FT TRANSMEM 431 451 POTENTIAL.
 FT TRANSMEM 464 484 POTENTIAL.
 FT TRANSMEM 536 556 POTENTIAL.
 FT TRANSMEM 580 600 POTENTIAL.
 FT TRANSMEM 616 636 POTENTIAL.
 FT TRANSMEM 650 670 POTENTIAL.
 FT REPEAT 38 67 ANK 1.
 FT REPEAT 73 102 ANK 2.
 FT REPEAT 104 130 ANK 3.
 FT REPEAT 159 188 ANK 4.
 FT CARBOHYD 337 337 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 416 416 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 560 560 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CONFLICT 739 742 EMGM -> GNGEM (IN REF. 3).
 SQ SEQUENCE 848 AA; 97354 MW; 1DBC9ZBC941DF416 CRC64;
 Query Match 3.5%; Score 139; DB 1; Length 848;
 Best Local Similarity 18.4%; Pred. No. 0.024;
 Matches 128; Conservative 96; Mismatches 222; Indels 248; Gaps 32;
 OY 152 VNAOCTDYYRGHSALHIAIEKRSLOCVKLV--ENGANV-----HAR----- 192
 DB LNVNCVD--YMGONMLQOLAVGNEHLEVTLLKKEMLARIGALLAISKGVRIVEAIL 122
 OY 193 -----ACGRFQKG-----OGTCFYGELPLSLACQKPMQVSYLL-- 229
 DB 123 NHGFAASKRLTLPSCDELDDDFYAYDEGTRSPDITPILAHCKQYEVHMLMK 182
 OY 230 ----ENPH-----OPASLOANDSOQNTVLAHV 253
 DB 183 GARIEPHDYFCCKGDCMEKORHDSFSRSHINAYKGLASPAVISTL--SSDPVLTAL 240
 OY 254 MISDMSAENIALVTSMYD-----GLLOAGARLC-PRVQLEDIRN--LQDL 295
 DB 241 L--SNEKLANIEKEFKNDYRKLKSMCKDFVGVYLD--LCRDEEVEALINDLESA 294
 OY 296 PPLKLAAGKIEIPRH--ILOREFSGLSHSRKPFEM--CYGPVSLYDLASDSC 351
 DB 295 EPL-----EVRHRAKSLSRVKLAIRYEVKRYVAHPNCOOQLTIWYE--NLSGLE 343
 OY 352 NSVLEIIAFHCKSPHRHRVVL-----EPNLKLOAKMDLIPKFL 393
 DB 344 ----QTIAIKC-----LVVLVALGUPFLAIGYWIAPCSLGLILRSP-----FM 384
 OY 394 NFLCLNLIYFITTAVAYHO-----PYLKQOAPHLKAEVGNMILTGHLIL-- 440
 DB 385 KEVAHAASEPIFLGLVFNASDRFEGITTLPMITVTDYPKQIFRYKTOFTWEMLIWV 444
 OY 441 -LGGIYLLVGLMW-----FMRHFEI-----WSF-----IDSY 469
 DB 445 VLGMMWSECKELMDEGPREYIIQLNNVLDFGMLSTIFIAFTARLAFQATQAQYVDSY 504
 OY 470 PELLFLFOALLTVVSOVLCFLAIEWLP-----LLVSLVGLMNLVLYTGTGFGHT 520
 DB 505 VQESDSEVTLPPELOYFTYARDK--LPSDPQIISBGLAIVAVLSFSIAVITLANESF 563
 OY 521 GIYSVWIOKVILRDLRLFLLYLVFLGFAVALVLSQEAWEPEAPTPGNATESVOPEMG 580
 DB 564 GPLQISLGRV-KDIFKRMVLEIMVFAPFMIGMFTLYSYLGAKV----- 607
 OY 581 QEDDEGNGAQRIILASLELFFETIGMELA-----FOEOLHFPGMVLILLALV 631
 DB 608 -----NAFTVESSEFTKLEVSIGLSEVTSVLKDYHKFTENIGY-----VLGIYV 656
 OY 632 LTYILLNMLIALMSETVNSVATDSMSIMKLOKA 665
 DB 657 TMVVVLLNMLIAMINSYOEIEDSDVEMKPARS 690
 RESULT 9

ANK1_HUMAN STANDARD: PRT: 1880 AA.
 ID ANK1_HUMAN
 AC P16157;
 DT 01-APR-1990 (rel. 14, Created)
 DT 01-APR-1990 (rel. 14, Last sequence update)
 DT 01-OCT-2000 (rel. 40, Last annotation update)
 DE ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).
 GN ANK1 OR ANK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
 RC TISSUE=Hematopoietic;
 RX MEDLINE=90158830; PubMed=2137557;
 RA Lux S.E., John K.M., Bennett V.;
 RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
 RT structure with homology to tissue-differentiation and cell-cycle
 RT control proteins.";
 RL Nature 344:36-42(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90175370; PubMed=1689849;
 RX Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,
 RA Cheung M.C., Kan Y.W., Palek J.;
 RT "cDNA sequence for human erythrocyte ankyrin";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
 RN [3]
 RP VARIANT HS IL6-462.
 RC MEDLINE=96225450; PubMed=8640229;
 RX Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
 RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekun A.,
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive
 RT hereditary spherocytosis.";
 RL Nat. Genet. 13:214-218(1996);
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
 CC ELEMENTS: BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
 CC NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN G85, AND TO THE
 CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
 CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
 CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
 CC PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY
 CC ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
 CC VARIANT 2.1.
 CC -1- PTM: REGULATED BY PHOSPHORYLATION.
 CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
 CC -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE
 CC HEREDITARY SPHEROCYTOSIS (HS).
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -----
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 CC -----
 CC EMBL: X16609; CAA34610.1; -
 CC EMBL: M28880; AAA1732.1; -
 CC PIR: S08275; SJHUK.
 CC PIR: A35049; A35049.
 CC HSSP: 000420; 1AMC.
 CC MIM: 182900; -
 CC InterPro: IPR000488; -
 CC InterPro: IPR000906; -
 CC InterPro: IPR002110; -
 CC Pfam: PF00791; Z05; 1.

DR Pfam: PF00023; ank: 22.
 DR Pfam: PF00531; death: 1.
 DR PROSITE: PS50088; ANK_REPEAT: 20.
 DR PROSITE: PS50297; ANK_REPEAT_REGION: 1.
 DR PROSITE: PS50017; DEATH_DOMAIN: 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Phosphorylation; Lipoprotein; Multigene family; Disease mutation;
 KW Elliptocytosis; Polymorphism.
 FT INIT_MER 0
 FT DOMAIN 1 826
 FT
 FT DOMAIN 827 1381
 FT
 FT DOMAIN 1382 1880
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 FT REPEAT 43 72
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 FT REPEAT 633 662
 FT REPEAT 666 695
 FT REPEAT 699 728
 FT REPEAT 732 761
 FT REPEAT 765 794
 FT DOMAIN 1402 1486
 FT VARSPLIC 1512 1873
 FT VARSPLIC 1874 1874
 FT VARSPLIC 1849 1880
 FT
 FT VARIANT 20 20
 FT
 FT VARIANT 462 462
 FT
 FT VARIANT 618 618
 FT
 FT VARIANT 749 749
 FT
 FT VARIANT 844 844
 FT
 FT VARIANT 1391 1391
 FT
 FT VARIANT 1285 1285
 FT
 FT VARIANT 1591 1591
 FT
 FT VARIANT 1698 1698
 FT
 FT CONFLICT 229 229
 FT CONFLICT 1345 1345
 SQ SEQUENCE 1880 AA; 206145 MW; 1C5F5E7BED1CD428 CRC64;

Query Match 3.4%; Score 138; DB 1; Length 1880;
 Best Local Similarity 22.8%; Pred.No. 0.079; Indels 110; Gaps 16;
 Matches 82; Conservative 45; Mismatches 122; Indels 110; Gaps 16;
 QY 134 CILPLQIDRD-----SGNQPPL-VNAOCTDYYR-----GHSALHI 169


```

CC -----
DR EMBL: 250142: CAA90497.1: -
DR HSSP: Q00420: IANC.
DR InterPro: IPR001594: -
DR InterPro: IPR002110: -
DR Pfam: PF00023: ank; 6.
DR Pfam: PF01529: zf-DHHC; 1.
DR PROSITE: PS50088: ANK_REPEAT; 1.
DR PROSITE: PS50088: ANK_REPEAT; 3.
DR PROSITE: PS50297: ANK_REPEAT_REGION; 1.
DR Hypothetical protein; ANK repeat; Repeat.
FT REPEAT 1 29 ANK 1.
FT REPEAT 33 62 ANK 2.
FT REPEAT 67 96 ANK 3.
FT REPEAT 100 129 ANK 4.
FT REPEAT 133 162 ANK 5.
FT REPEAT 166 196 ANK 6.
SQ SEQUENCE 642 AA: 72521 MW: C83584A3300BDDA0 CRC64;

```

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Query Match 3.3% Score 133.5; DB 1; Length 642;
Best Local Similarity 21.0%; Pred. No. 0.042;
Matches 95; Conservative 71; Mismatches 136; Indels 151; Gaps 23;

```

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QY 152 VNAQCTDDYRGSHALHIAIEKRSLOCVKLLVNGANVHARACGRFGOGTCFYGEL 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 25 IDVNATDE--GGATLHMAALNQOIPICKFLEHGADVAIG-----GDL 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 ---PLSLACTKQMDVSVLLLENPHOPASIQATDSOGNTVLAHVAISD----- 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 QAAPIHMAKRSGSVKTVHLYOHGADPL--LKDQGFNCLHVAHVASPLVYLLHLD 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 258 ---NSANIALVTSMDG-----LLOAGARLCPTVLEDINLQDLPFLKLAK 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 125 ISVDLRDDQHTPLMASHYGNPITNCLLRGADVAIDE-----DKMPLHMSIYG 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 305 GKIEIFRHLQREFSGL-----SHLSRKF-TEWCY-GPVARS-LYDLASVDS--CEEN 352
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 178 GNLCKMKLLIKE--CGICTAVANLSGQIKFPWALASELRVSHLFRKQALISNGLKVKET 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 353 SVLEIIFAFCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLCMLIYFITTAAVYHQ 412
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 236 SE-----EP-----EKWVVSRSKQFSOKTPIICFL----- 262
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 413 PTLKQAARHLKAQVNSMLTGHILIG---GIYLLVGLDM-YFWR----- 457
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 263 -----SFTITGVFFIMSICPMVSLIAPIMYITFKYITTCIHANI 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 458 ---HVEFIWISFIDSYELLFLF---QALLTVVSQVLCFLAIEWYLDPLVASLVGLMLNL 511
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 307 DIVHFEYLEPFLAGISISIFFWWCHSLIYVKTLPKIPKLSLLFLVLSFTCIG---L 362
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 512 YTRGFQHTG---IYSV-----IOKVLRDL 535
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 363 YVTAFAQNGVYDKIGAVVQRREEISKLDKDL 395
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 12
TRP6_MOUSE STRAND: PRT; 930 AA.
AC Q61143: Q922J1:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TRANSIENT RECEPTOR POTENTIAL CHANNEL 6 (CALCIUM ENTRY CHANNEL).
GN TRP6 OR TRP6 OR TRP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98037793; PubMed=9368034;

```

```

RA Boulay G., Zhu X., Peyton M., Jiang M., Hurst R., Stefani E.,
RA Birbaumer L.:
RT "Cloning and expression of a novel mammalian homolog of Drosophila
RT transient receptor potential (trp) involved in calcium entry secondary
RT to activation of receptors coupled by the Gq class of G protein.";
RL J. Biol. Chem. 272:29672-29680(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA/2;
RX MEDLINE=99158172; PubMed=10050885;
RA Buess M., Engler O., Hirsch H.H., Moroni C.;
RT "Search for oncogenic regulators in an autocrine tumor model using
RT differential display PCR: identification of novel candidate genes
RT including the calcium channel mtrp6.";
RL Oncogene 18:1487-1494(1999).
RN [3]
RP SEQUENCE OF 631-739 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96234226; PubMed=8646775;
RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
RA Birbaumer L.;
RT "trp, a novel mammalian gene family essential for agonist-activated
RT capacitative Ca2+ entry.";
RL Cell 85:661-671(1996).
CC -I- FUNCTION: NONSELECTIVE CAPACITATIVE CALCIUM ENTRY CHANNEL SUBUNIT.
CC MEDIATES CALCIUM ENTRY STIMULATED BY A G-PROTEIN COUPLED RECEPTOR
CC BUT NOT BY INTRACELLULAR CALCIUM STORE DEPLETION. ACTIVATED BY
CC DIACYLGLYCEROL (DAG) IN A MEMBRANE-DELIMITED FASHION INDEPENDENTLY
CC OF PROTEIN KINASE C. IT IS PERMEABLE FOR CALCIUM, CESIUM, SODIUM,
CC POTASSIUM AND MAGNESIUM.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -I- TISSUE SPECIFICITY: LUNG AND BRAIN.
CC -I- PTM: N-GLYCOSYLATED.
CC -I- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
CC -I- SIMILARITY: CONTAINS 3 ANK REPEATS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U49069: AAC06146.1: -
DR EMBL: AF057748: AAC64394.1: -
DR MGD: MGI:109523; Trp6.
DR InterPro: IPR002110; -
DR InterPro: IPR002153; -
DR Pfam: PF00023; ank; 2.
DR PRINTS: PR01097; TRNSRECEPTRP.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Ionic channel; transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Glycoprotein.
FT TRANSMEM 406 426 POTENTIAL.
FT TRANSMEM 438 458 POTENTIAL.
FT TRANSMEM 467 507 POTENTIAL.
FT TRANSMEM 521 541 POTENTIAL.
FT TRANSMEM 592 612 POTENTIAL.
FT TRANSMEM 636 656 POTENTIAL.
FT TRANSMEM 706 726 POTENTIAL.
FT REPEAT 131 160 ANK 1.
FT REPEAT 162 188 ANK 2.
FT REPEAT 217 246 ANK 3.
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 727 727 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 3 56 MISSING (IN REF. 2).
FT CONFLICT 105 105 V -> A (IN REF. 2).

```


FT	DOMAIN	273	309	EGF-LIKE 7,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	311	350	EGF-LIKE 8,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	352	388	EGF-LIKE 9,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	389	427	EGF-LIKE 10,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	429	470	EGF-LIKE 11,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	472	508	EGF-LIKE 12,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	510	546	EGF-LIKE 13,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	548	584	EGF-LIKE 14,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	586	622	EGF-LIKE 15,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	622	656	EGF-LIKE 16,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	658	686	EGF-LIKE 17,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	688	724	EGF-LIKE 18,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	726	762	EGF-LIKE 19,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	764	800	EGF-LIKE 20,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	803	839	EGF-LIKE 21,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	841	877	EGF-LIKE 22,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	878	924	EGF-LIKE 23,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	926	962	EGF-LIKE 24,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	964	1000	EGF-LIKE 25,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	1002	1040	EGF-LIKE 26,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	1042	1081	EGF-LIKE 27,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	1083	1122	EGF-LIKE 28,	CALCIUM-BINDING	(POTENTIAL)
FT	DOMAIN	1126	1167	EGF-LIKE 29,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1168	1208	LIN/NOTCH 1,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1209	1242	LIN/NOTCH 2,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1243	1282	LIN/NOTCH 3,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1268	1307	ANK 1,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1343	1382	ANK 2,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1407	1446	ANK 3,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1472	1511	ANK 4,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1537	1576	ANK 5,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1602	1641	ANK 6,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1667	1706	ANK 7,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1732	1771	ANK 8,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1797	1836	ANK 9,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1862	1901	ANK 10,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1927	1966	ANK 11,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	1992	2031	ANK 12,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2057	2096	ANK 13,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2122	2161	ANK 14,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2187	2226	ANK 15,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2252	2291	ANK 16,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2317	2356	ANK 17,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2382	2421	ANK 18,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2447	2486	ANK 19,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2512	2551	ANK 20,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2577	2616	ANK 21,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2642	2681	ANK 22,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2707	2746	ANK 23,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2772	2811	ANK 24,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2837	2876	ANK 25,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2902	2941	ANK 26,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	2967	3006	ANK 27,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3032	3071	ANK 28,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3097	3136	ANK 29,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3162	3201	ANK 30,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3227	3266	ANK 31,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3292	3331	ANK 32,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3357	3396	ANK 33,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3422	3461	ANK 34,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3487	3526	ANK 35,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3552	3591	ANK 36,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3617	3656	ANK 37,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3682	3721	ANK 38,	CALCIUM-BINDING	(POTENTIAL)
FT	REPEAT	3747	3786	ANK 39,	CALCIUM-BINDING	(POTENTIAL)</

	FT	DISULFID	590	601	BY SIMILARITY.
	FT	DISULFID	595	610	BY SIMILARITY.
	FT	DISULFID	612	621	BY SIMILARITY.
	FT	DISULFID	626	637	BY SIMILARITY.
	FT	DISULFID	631	646	BY SIMILARITY.
	FT	DISULFID	648	655	BY SIMILARITY.
	FT	DISULFID	662	669	BY SIMILARITY.
	FT	DISULFID	664	674	BY SIMILARITY.
	FT	DISULFID	676	685	BY SIMILARITY.
	FT	DISULFID	692	703	BY SIMILARITY.
	FT	DISULFID	697	712	BY SIMILARITY.
	FT	DISULFID	714	723	BY SIMILARITY.
	FT	DISULFID	730	741	BY SIMILARITY.
	FT	DISULFID	735	750	BY SIMILARITY.
	FT	DISULFID	752	761	BY SIMILARITY.
	FT	DISULFID	768	779	BY SIMILARITY.
	FT	DISULFID	773	788	BY SIMILARITY.
	FT	DISULFID	790	799	BY SIMILARITY.
	FT	DISULFID	807	818	BY SIMILARITY.
	FT	DISULFID	812	827	BY SIMILARITY.
	FT	DISULFID	829	838	BY SIMILARITY.
	FT	DISULFID	845	856	BY SIMILARITY.
	FT	DISULFID	850	865	BY SIMILARITY.
	FT	DISULFID	867	876	BY SIMILARITY.
	FT	DISULFID	882	903	BY SIMILARITY.
	FT	DISULFID	897	912	BY SIMILARITY.
	FT	DISULFID	914	923	BY SIMILARITY.
	FT	DISULFID	930	941	BY SIMILARITY.
	FT	DISULFID	935	950	BY SIMILARITY.
	FT	DISULFID	952	961	BY SIMILARITY.
	FT	DISULFID	968	979	BY SIMILARITY.
	FT	DISULFID	973	988	BY SIMILARITY.
	FT	DISULFID	990	999	BY SIMILARITY.
	FT	DISULFID	1006	1019	BY SIMILARITY.
	FT	DISULFID	1011	1028	BY SIMILARITY.
	FT	DISULFID	1030	1039	BY SIMILARITY.
	FT	DISULFID	1046	1057	BY SIMILARITY.
	FT	DISULFID	1051	1069	BY SIMILARITY.
	FT	DISULFID	1071	1080	BY SIMILARITY.
	FT	DISULFID	1087	1098	BY SIMILARITY.
	FT	DISULFID	1092	1110	BY SIMILARITY.
	FT	DISULFID	1112	1121	BY SIMILARITY.
	FT	DISULFID	1130	1142	BY SIMILARITY.
	FT	DISULFID	1136	1155	BY SIMILARITY.
	FT	DISULFID	1157	1166	BY SIMILARITY.

Query Match 3.2% Score 129; DB 1; Length 1964;
Best Local Similarity 25.5%, Pred. No. 0.37,
Matches 72; Conservative 37; Pident matches 103; Indels 70; Gaps 12;

```
OY      94 LPEVLSKTSKYLTDESEY-----TEGSGNGKCLMKAV----LNKKDGVNACILPLQIDRDS   145
          ||| |           :|||             |:|||         | :| |       |
DB     1553 LPQAAMLPTRPCECBESBVLVDPTCGPDGTVPPLMSANFCGGVOSTTGASPORLGL-----*1605
OY      146 GNQP-----LVNAOCTDIYY--RGSHALHIAIEKRSLOCVKLIVENGAN-----    188
          ||| |           |::|            |::| |         |::| |       |
DB     1606 GNLEWEPILLDGACPQATVTGTFPHLLARFSRPAPRARLLLEGANGPNQDRAGRTP   1665
OY      189 -----VAHRACGRFFOKGCOTCF-----YFGELPSLAACIQMDIVSYTLENPHOPASL   238
          ||| |           |||              |::| |         |::| |       |
DB     1666 IHTAAVAADAREVCOLLASROTSDARTEDGTTPLMLARLAVEDVELLIA---ARADV   1722
OY      239 QATDSOGNTVFHLAIWMISNSAENIALVYSMTDGLLAGAGARCPLYOULEDINLDIPL   298
          |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
DB     1723 KARDRKGTALTMAAAVNARAAR-----SIIAQCAD-----KDAODSRQETPL   1766
OY      299 FLAKREGKIETFRHILO-----REFSQLS--HSRKETE W   331
          |||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
DB     1767 FLAAREGAVEVAQLLELGARGDLDDQGLARGDVVARQRSHW   1808
```

RESULT 14
SW14_YEAST

ID	SW14 YEAST	STANDARD:	PRT:	1093 AA.
AC	P25302;			
AD	01-MAY-1992 (Rel. 22, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	REGULATORY PROTEIN SW14 (CELL-CYCLE BOX FACTOR, CHAIN SW14)			
DE	(ART1 PROTEIN).			
GN	SW14 OR ART1 OR YER11C.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.			
NCBI	taxid:4932;			
NCBI	taxid:4932;			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90098089; PubMed=2689885;			
RA	Andrews B.J., Herskowitz I.,			
RT	"The yeast SW14 protein contains a present in developmental			
RT	regulators and is part of a complex involved in cell-cycle-dependent			
RL	transcription."			
RL	Nature 342:830-833(1989).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RA	STRAIN=S288C / AB972;			
RA	Dierich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,			
RA	Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,			
RA	Chung E., Duncan M., Guzman E., Hartwell G., Hunnicke-Smith S.,			
RA	Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,			
RA	Mosedale D., Nakshatra K., Namlath A., Norgren R., Oefner P., Oh C.,			
RA	Petel F.X., Roberts D., Sehgal P., Schramm S., Shogren T., Smith V.,			
RA	Taylor P., Wei Y., Yellon M., Botstein D., Davis R.M.			
RN	Submitted (DEC-1994) to the EMBL/genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 845-1093 FROM N.A.			
RX	MEDLINE=93360904; PubMed=8353657;			
RA	Daniel J.;			
RT	"Potentially rapid walking in cellular regulatory networks using the			
RT	gene-gene interference method in yeast."			
RL	Mol. Gen. Genet. 240:245-257(1993)			
CC	-I- FUNCTION: PART OF A COMPLEX INVOLVED IN CELL-CYCLE-DEPENDENT			
CC	TRANSCRIPTION. SW14 AND SW16 ARE REQUIRED FOR FORMATION OF THE			
CC	CELL-CYCLE BOX FACTOR-DNA COMPLEX. THE REPEATED ELEMENT IN THE			
CC	UPSTREAM REGION OF HO (5'-CACCAAA-3') IS CALLED THE CELL CYCLE			
CC	BOX (CCB).			
CC	-I- SUBUNIT: SBF CONTAINS SW16 AND SW14.			
CC	-I- SIMILARITY: CONTAINS 2 ANK REPEATS.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL: X51606; CAA35949.1; -			
DR	EMBL: U18916; AAC03209.1; -			
DR	PIR: S07106; S07106.			
DR	PIR: S35260; S35260.			
DR	TRANSFAC: T00775; -			
DR	SGD: S0000913; SW14.			
DR	InterPro: IPR002110; -			
DR	Pfam: PF00023; ank; 2.			
DR	PROSITE: PS50088; ANK_REPEAT; 2.			
DR	PROSITE: PS50297; ANK_REPEAT; 2.			
KW	Transcription regulation; DNA-binding; ANK repeat; Repeat.			
FT	DOMAIN 37 138			
FT	DOMAIN 37 138			
FT	REPEAT 520 549			
FT	REPEAT 520 549			
FT	REPEAT 641 670			
FT	REPEAT 641 670			
FT	CONFLICT 175 175 R -> T (IN REF. 1).			
FT	CONFLICT 431 431 V -> I (IN REF. 1).			
FT	CONFLICT 1054 1054 A -> L (IN REF. 1).			
FT	CONFLICT 1054 1054 A -> L (IN REF. 1).			
FT	CONFLICT 3 846 MISSING (IN REF. 2).			

SQ SEQUENCE 1093 AA; 123806 MW; 40EA2EA7732687A9 CRC64;
 Query Match 3.2%; Score 128.5; DB 1; Length 1093;
 Best Local Similarity 20.8%; Pred. No. 0.19;
 Matches 74; Conservative 48; Mismatches 134; Indels 99; Gaps 14;
 QY 10 FILETLDDGGQEDSGFADRGKLDPSGGLPDMESQFQEDGRKAPQIRV-----56
 Db 357 FHHSMWSDITNGNSKKRRKKLNQSN-----EQGFYNQOEKIQRFHKLKQPLMQSPNP 411
 QY 57 -----NLVRRKGTGASQDPDRFRDRLFNAVSVGVPEDLAGLEPIYSKT 101
 Db 412 NDHNEHYCDMSGNNNNNTVANSNGSIEVFSSENDNSMNNSSMPFSGAGNTSSOKRL 471
 QY 102 SKYLDSEYTEGSGTKCTLMKAVLNLMKDVNACILPLLDIORDSGNPOPL-----151
 Db 472 EKKMTQDGYEKQ-----TITLTSSRSRDDVDQALLATLTPAPKN 510
 QY 152 --VNAQCTDDYRCHGSAHLIAIEKRSLOCVLLVENGANVHARACGRF-FQGGGCTCFYF 208
 Db 511 FNIINEID--QGHTPLPMATAMANIPLIMLTLLNAN--ALQCNKLGFCNICIKTSIFYN 565
 QY 209 GELPLSLACTKQ--WDVVSYLENPHQPASLQATDSQGNVTALVWISQNSAENIALY 266
 Db 566 N-----CKENAFDEIISILK-----ICLTIPDVNGRLPFHYLLSELVSNNKSNPMT 612
 QY 267 TSMYDG-LIQAG-----ARLCPTVQLEDIRNLQDLPLPLKLAKEGKIEIFRHIL 314
 Db 613 KSYMDSITLSGGQDYNLKTKICLNMQ-DNIGN-----IPLHLISALNLMPEVYNRLV 662
 RESULT 15
 NOTCH_DROME STANDARD; PRT; 2703 AA.
 ID NOTCH_DROME
 AC P07207; P04154;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR.
 GN N.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN 11
 RP SEQUENCE FROM N.A.
 RX Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
 RT "Nucleotide sequence from the neurogenic locus notch implies a gene
 RT product that shares homology with proteins containing EGF-like
 RT repeats."
 RL Cell 43:567-581(1985).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RX MEDLINE=87064624; PubMed=3097517;
 RA Kidd S., Kelley M.R., Young M.W.;
 RT "Sequence of the notch locus of Drosophila melanogaster: relationship
 RT of the encoded protein to mammalian clotting and growth factors."
 RL Mol. Cell. Biol. 6:3094-3108(1986).
 RN 131
 RP SEQUENCE OF 2505-2611 FROM N.A.
 RX MEDLINE=85099329; PubMed=2981631;
 RA Wharton K.A., Vedvodnitch B., Finnerty V.G., Artavanis-Tsakonas S.;
 RT "opa: a novel family of transcribed repeats shared by the Notch locus
 RT and other developmentally regulated loci in D. melanogaster."
 RL Cell 40:55-62(1985).
 RN 141
 RP SEQUENCE OF 1-8 FROM N.A.
 RX MEDLINE=87257846; PubMed=3037327;
 RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;

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RT "Restriction of P-element insertions at the Notch locus of Drosophila
RL melanogaster."
RN Mol. Cell. Biol. 7:1545-1548(1987).
RP [5]
RA REVIEW.
RT Harris W.A.:
RL "Many cell types specified by Notch function."
RT Curr. Biol. 1:120-122(1991).
CC -1- FUNCTION: NOTCH PROTEIN IS ESSENTIAL FOR PROPER DIFFERENTIATION OF
CC ECTODERM.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO
CC THE INNER PART OF EMBRIO IS ONE OF THE FIRST STEPS OF CNS
CC DEVELOPMENT IN INSECTS, THIS PROCESS IS UNDER CONTROL OF THE
CC NEUROGENIC GENES.
CC -1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M16152; AAB59220.1; -.
DR EMBL: M16153; AAB59220.1; JOINED.
DR EMBL: M16149; AAB59220.1; JOINED.
DR EMBL: M16150; AAB59220.1; JOINED.
DR EMBL: M16151; AAB59220.1; JOINED.
DR EMBL: M13689; AAA28725.1; -.
DR EMBL: M13689; AAA28725.1; JOINED.
DR EMBL: K03507; AAA28725.1; JOINED.
DR EMBL: M12175; AAA74496.1; -.
DR EMBL: M16025; AAA28726.1; -.
DR PIR: A24420; A24420.
DR PIR: A24768; A24768.
DR PIR: A05267; A05267.
DR HSSP: P00740; 11YA.
DR Flybase: FBgn004647; N.
DR InterPro: IPR000152; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR000800; -.
DR InterPro: IPR001438; -.
DR InterPro: IPR001881; -.
DR InterPro: IPR002110; -.
DR Pfam: PF00008; EGF; 36.
DR Pfam: PF00023; ank; 6.
DR Pfam: PF00066; notch; 3.
DR PRINTS: PR00010; EGFBLD.
DR PROSITE: PS30088; ANK_REPEAT; 5.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 22.
DR PROSITE: PS00022; EGF_1; 34.
DR PROSITE: PS01186; EGF_2; 28.
DR PROSITE: PS01187; EGF_CA; 22.
KW Differentiation; Neurogenesis; Repeat; ANK repeat; EGF-like domain;
KW Transmembrane; Signal; Glycoprotein.
KW SIGNAL
FT CHAIN 1 44 POTENTIAL.
FT DOMAIN 45 2703 NEUROGENIC LOCUS NOTCH PROTEIN.
FT TRANSMEM 45 1745 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1767 1766 POTENTIAL.
FT DOMAIN 1767 2703 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 58 95 EGF-LIKE 1.
FT DOMAIN 96 136 EGF-LIKE 1.
FT DOMAIN 139 176 EGF-LIKE 2.
FT DOMAIN 177 215 EGF-LIKE 3.
FT DOMAIN 217 253 EGF-LIKE 4.
FT DOMAIN 255 291 EGF-LIKE 5.
FT DOMAIN 293 329 EGF-LIKE 6.
FT DOMAIN 293 329 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 331 370 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 372 408 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 409 447 EGF-LIKE 10.
FT DOMAIN 449 486 EGF-LIKE 11.
FT DOMAIN 488 524 EGF-LIKE 12.
FT DOMAIN 526 562 EGF-LIKE 13.
FT DOMAIN 564 600 EGF-LIKE 14.
FT DOMAIN 602 637 EGF-LIKE 15.
FT DOMAIN 639 675 EGF-LIKE 16.
FT DOMAIN 677 713 EGF-LIKE 17.
FT DOMAIN 715 751 EGF-LIKE 18.
FT DOMAIN 753 789 EGF-LIKE 19.
FT DOMAIN 791 827 EGF-LIKE 20.
FT DOMAIN 829 865 EGF-LIKE 21.
FT DOMAIN 867 905 EGF-LIKE 22.
FT DOMAIN 907 944 EGF-LIKE 23.
FT DOMAIN 946 982 EGF-LIKE 24.
FT DOMAIN 984 1020 EGF-LIKE 25.
FT DOMAIN 1022 1058 EGF-LIKE 26.
FT DOMAIN 1060 1096 EGF-LIKE 27.
FT DOMAIN 1098 1134 EGF-LIKE 28.
FT DOMAIN 1136 1181 EGF-LIKE 29.
FT DOMAIN 1183 1219 EGF-LIKE 30.
FT DOMAIN 1221 1257 EGF-LIKE 31.
FT DOMAIN 1259 1295 EGF-LIKE 32.
FT DOMAIN 1297 1335 EGF-LIKE 33.
FT DOMAIN 1337 1373 EGF-LIKE 34.
FT DOMAIN 1375 1412 EGF-LIKE 35.
FT DOMAIN 1415 1451 EGF-LIKE 36.
FT REPEAT 1475 1513 LIN/NOTCH 1.
FT REPEAT 1514 1553 LIN/NOTCH 2.
FT REPEAT 1554 1593 LIN/NOTCH 3.
FT REPEAT 1901 1945 ANK 1.
FT REPEAT 1950 1979 ANK 2.
FT REPEAT 1983 2013 ANK 3.
FT REPEAT 2017 2046 ANK 4.
FT REPEAT 2050 2079 ANK 5.
FT REPEAT 2083 2112 ANK 6.
FT DOMAIN 2538 2568 POLY-GLN (OPA-REPEAT).
FT DISULFID 62 73 BY SIMILARITY.
FT DISULFID 67 83 BY SIMILARITY.
FT DISULFID 85 94 BY SIMILARITY.
FT DISULFID 100 111 BY SIMILARITY.
FT DISULFID 105 124 BY SIMILARITY.
FT DISULFID 126 135 BY SIMILARITY.
FT DISULFID 143 154 BY SIMILARITY.
FT DISULFID 148 164 BY SIMILARITY.
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FT DISULFID 476 485 BY SIMILARITY.
FT DISULFID 492 503 BY SIMILARITY.

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FT DISULFID 568 579 BY SIMILARITY.
FT DISULFID 573 588 BY SIMILARITY.
FT DISULFID 590 599 BY SIMILARITY.
FT DISULFID 606 616 BY SIMILARITY.
FT DISULFID 611 625 BY SIMILARITY.
FT DISULFID 627 636 BY SIMILARITY.
FT DISULFID 643 654 BY SIMILARITY.
FT DISULFID 648 663 BY SIMILARITY.
FT DISULFID 665 674 BY SIMILARITY.
FT DISULFID 681 692 BY SIMILARITY.
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Query Match 3 18; Score 124.5; DB 1; Length 2703;

Best Local Similarity 23.98; Pred. No. 1.2; Mismatches 115; Indels 77; Gaps 15;

Matches 75; Conservative 47; Mismatches 115; Indels 77; Gaps 15;

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QY 39 MESQFQGERKRFAPQIRVNINLRKQ--TGASQDPNRFDRD-----LFNAVSRG-- 86
DB 1856 MYSEYEADQQRWMSQAHLDVNVYRAIMTPRAHQDGGKHVDARGPGCLTPMLTAAYRGGS 1915
QY 87 --VPEDLAGLPEYLSKTSKYLD-----SEYEGSTGKTCIMKAVLNKQGVNACILP 137
DB 1916 LPTGEDIEENNED---STAQVISDLAOGAELNATMDKTGETSLHLARFARADAKRRL- 1971
QY 138 LQIDRDGPNQPLVNAOCTDDYRGHSALHTAIEKRSLOCVKLIYENGA-NVHARACGR 196
DB 1972 -----DAG-----ADANCODN--TGRTPHAAVNAADAMGVFOILLRNRYTNLNAR---- 2014
QY 197 FPOKGGCTCFYEGELPLSLACTKQMDVVSYLENPHOPASLOATDSOGNTVLLHALMIS 256
DB 2015 -----MHDGTPLLIARLAIEGWEDLIT---ADADRMAADNSGKTALHMAAAYN 2062
QY 257 DNSAENIALVTSMYDGLQAGARLCPTVOLEDIRNLQDLTPKLAKKEGKIETFRHIL-- 314
DB 2063 NTEAVNI-----LMHHAN-----RDADKDETPLELAREGSYEACKALLDN 2106
QY 315 --QREFSGLSHLR 326
DB 2107 FANREIT--DHMDR 2118
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Job time: 131 sec